

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/618, 143A  
Source: TFW16  
Date Processed by STIC: 10/12/2006

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/618,143A

TIME: 15:56:29

Input Set : A:\078-us1.ST25.txt

Output Set: N:\CRF4\10122006\J618143A.raw

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3 <110> APPLICANT: Paz Einat, Louis Deiss, and Ruth Maya
5 <120> TITLE OF INVENTION: ISOCITRATE DEHYDROGENASE AND USES THEREOF
7 <130> FILE REFERENCE: 67723-A; 078-US1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/618,143A
C--> 10 <141> CURRENT FILING DATE: 2003-07-11
12 <150> PRIOR APPLICATION NUMBER: 60/395364
13 <151> PRIOR FILING DATE: 2002-07-11
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2301
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (247)..(1491)
29 <400> SEQUENCE: 1
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34 tgtactttaa accggataaa ctgggctgtc tggcaggcga taaactacat tcagttgagt      180
36 ctgcaagact gggaggaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa      240
38 gtcaaa atg tcc aaa aaa atc agt ggc ggt tct gtg gta gag atg caa      288
39 Met Ser Lys Lys Ile Ser Gly Gly Ser Val Val Glu Met Gln
40 1 5 10
42 gga gat gaa atg aca cga atc att tgg gaa ttg att aaa gag aaa ctc      336
43 Gly Asp Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu
44 15 20 25 30
46 att ttt ccc tac gtg gaa ttg gat cta cat agc tat gat tta ggc ata      384
47 Ile Phe Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile
48 35 40 45
50 gag aat cgt gat gcc acc aac gac caa gtc acc aag gat gct gca gaa      432
51 Glu Asn Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu
52 50 55 60
54 gct ata aag aag cat aat gtt ggc gtc aaa tgt gcc act atc act cct      480
55 Ala Ile Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro
56 65 70 75
58 gat gag aag agg gtt gag gag ttc aag ttg aaa caa atg tgg aaa tca      528
59 Asp Glu Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser
60 80 85 90
62 cca aat ggc acc ata cga aat att ctg ggt ggc acg gtc ttc aga gaa      576
63 Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu
64 95 100 105 110
67 gcc att atc tgc aaa aat atc ccc cgg ctt gtg agt gga tgg gta aaa      624

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68	Ala	Ile	Ile	Cys	Lys	Asn	Ile	Pro	Arg	Leu	Val	Ser	Gly	Trp	Val	Lys	
69					115					120					125		
71	cct	atc	atc	ata	ggt	cgt	cat	gct	tat	ggg	gat	caa	tac	aga	gca	act	672
72	Pro	Ile	Ile	Ile	Gly	Arg	His	Ala	Tyr	Gly	Asp	Gln	Tyr	Arg	Ala	Thr	
73					130					135					140		
75	gat	ttt	gtt	gtt	cct	ggg	cct	gga	aaa	gta	gag	ata	acc	tac	aca	cca	720
76	Asp	Phe	Val	Val	Pro	Gly	Pro	Gly	Lys	Val	Glu	Ile	Thr	Tyr	Thr	Pro	
77					145					150					155		
79	agt	gac	gga	acc	caa	aag	gtg	aca	tac	ctg	gta	cat	aac	ttt	gaa	gaa	768
80	Ser	Asp	Gly	Thr	Gln	Lys	Val	Thr	Tyr	Leu	Val	His	Asn	Phe	Glu	Glu	
81					160					165					170		
83	ggt	ggt	ggt	gtt	gcc	atg	ggg	atg	tat	aat	caa	gat	aag	tca	att	gaa	816
84	Gly	Gly	Gly	Val	Ala	Met	Gly	Met	Tyr	Asn	Gln	Asp	Lys	Ser	Ile	Glu	
85	175					180					185					190	
87	gat	ttt	gca	cac	agt	tcc	ttc	caa	atg	gct	ctg	tct	aag	ggt	tgg	cct	864
88	Asp	Phe	Ala	His	Ser	Ser	Phe	Gln	Met	Ala	Leu	Ser	Lys	Gly	Trp	Pro	
89					195					200					205		
91	ttg	tat	ctg	agc	acc	aaa	aac	act	att	ctg	aag	aaa	tat	gat	ggg	cgt	912
92	Leu	Tyr	Leu	Ser	Thr	Lys	Asn	Thr	Ile	Leu	Lys	Lys	Tyr	Asp	Gly	Arg	
93					210					215					220		
95	ttt	aaa	gac	atc	ttt	cag	gag	ata	tat	gac	aag	cag	tac	aag	tcc	cag	960
96	Phe	Lys	Asp	Ile	Phe	Gln	Glu	Ile	Tyr	Asp	Lys	Gln	Tyr	Lys	Ser	Gln	
97					225					230					235		
99	ttt	gaa	gct	caa	aag	atc	tgg	tat	gag	cat	agg	ctc	atc	gac	gac	atg	1008
100	Phe	Glu	Ala	Gln	Lys	Ile	Trp	Tyr	Glu	His	Arg	Leu	Ile	Asp	Asp	Met	
101					240					245					250		
103	gtg	gcc	caa	gct	atg	aaa	tca	gag	gga	ggc	ttc	atc	tgg	gcc	tgt	aaa	1056
104	Val	Ala	Gln	Ala	Met	Lys	Ser	Glu	Gly	Gly	Phe	Ile	Trp	Ala	Cys	Lys	
105	255					260					265					270	
107	aac	tat	gat	ggt	gac	gtg	cag	tcg	gac	tct	gtg	gcc	caa	ggg	tat	ggc	1104
108	Asn	Tyr	Asp	Gly	Asp	Val	Gln	Ser	Asp	Ser	Val	Ala	Gln	Gly	Tyr	Gly	
109					275					280					285		
111	tct	ctc	ggc	atg	atg	acc	agc	gtg	ctg	gtt	tgt	cca	gat	ggc	aag	aca	1152
112	Ser	Leu	Gly	Met	Met	Thr	Ser	Val	Leu	Val	Cys	Pro	Asp	Gly	Lys	Thr	
113					290					295					300		
115	gta	gaa	gca	gag	gct	gcc	cac	ggg	act	gta	acc	cgt	cac	tac	cgc	atg	1200
116	Val	Glu	Ala	Glu	Ala	Ala	His	Gly	Thr	Val	Thr	Arg	His	Tyr	Arg	Met	
117					305					310					315		
119	tac	cag	aaa	gga	cag	gag	acg	tcc	acc	aat	ccc	att	gct	tcc	att	ttt	1248
120	Tyr	Gln	Lys	Gly	Gln	Glu	Thr	Ser	Thr	Asn	Pro	Ile	Ala	Ser	Ile	Phe	
121					320					325					330		
123	gcc	tgg	acc	aga	ggg	tta	gcc	cac	aga	gca	aag	ctt	gat	aac	aat	aaa	1296
124	Ala	Trp	Thr	Arg	Gly	Leu	Ala	His	Arg	Ala	Lys	Leu	Asp	Asn	Asn	Lys	
125	335					340					345					350	
127	gag	ctt	gcc	ttc	ttt	gca	aat	gct	ttg	gaa	gaa	gtc	tct	att	gag	aca	1344
128	Glu	Leu	Ala	Phe	Phe	Ala	Asn	Ala	Leu	Glu	Glu	Val	Ser	Ile	Glu	Thr	
129					355					360					365		
131	att	gag	gct	ggc	ttc	atg	acc	aag	gac	ttg	gct	gct	tgc	att	aaa	ggt	1392
132	Ile	Glu	Ala	Gly	Phe	Met	Thr	Lys	Asp	Leu	Ala	Ala	Cys	Ile	Lys	Gly	

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135 tta ccc aat gtg caa cgt tct gac tac ttg aat aca ttt gag ttc atg      1440
136 Leu Pro Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met
137          385          390          395
139 gat aaa ctt gga gaa aac ttg aag atc aaa cta gct cag gcc aaa ctt      1488
140 Asp Lys Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu
141          400          405          410
143 taa gttcatacct gagctaagaa ggataattgt cttttggttaa ctaggtctac      1541
145 aggtttacat ttttctgtgt tacactcaag gataaaggca aaatcaattt tgtaatttgt      1601
147 ttagaagcca gagtttatct tttctataag tttacagcct ttttcttata tatacagtta      1661
149 ttgccacctt tgtgaacatg gcaagggact tttttacaat ttttatttta ttttctagta      1721
151 ccagcctagg aattcggtta gtactcattt gtattcactg tcactttttc tcatgttcta      1781
153 attataaatg accaaaatca agattgctca aaagggtaaa tgatagccac agtattgctc      1841
155 cctaaaatat gcataaagta gaaattcact gccttcccct cctgtccatg acctggggca      1901
157 caggggaagt ctggtgtcat agatatcccg ttttgtgagg tagagctgtg cattaaactt      1961
159 gcacatgact ggaacgaagt aggagtgcaa ctcaaagtgt ttgaagatac tgcagtcatt      2021
161 tttgtaaaga ccttgctgaa tgtttccaat agactaaata ctgtttaggc cgcaggagag      2081
163 tttggaatcc ggaataaata ctacctggag gtttgtcctc tccatttttc tctttctcct      2141
165 cctggcctgg cctgaatatt atactactct aaatagcata tttcatccaa gtgcaataat      2201
167 gtaagctgaa tcttttttgg acttctgctg gcctgtttta tttcttttat ataaatgtga      2261
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173 <211> LENGTH: 414
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 2
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183 Glu Met Thr Arg Ile Ile Trp Glu Leu Ile Lys Glu Lys Leu Ile Phe
184          20          25          30
187 Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn
188          35          40          45
191 Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile
192          50          55          60
195 Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu
196 65          70          75          80
199 Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn
200          85          90          95
203 Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile
204          100          105          110
207 Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys Pro Ile
208          115          120          125
211 Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr Asp Phe
212          130          135          140
215 Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp
216 145          150          155          160
219 Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly
220          165          170          175
223 Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe

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224          180          185          190
227 Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr
228          195          200          205
231 Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys
232          210          215          220
235 Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu
236 225          230          235          240
239 Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala
240          245          250          255
243 Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr
244          260          265          270
247 Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu
248          275          280          285
251 Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu
252          290          295          300
255 Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln
256 305          310          315          320
259 Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp
260          325          330          335
263 Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu
264          340          345          350
267 Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu
268          355          360          365
271 Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro
272          370          375          380
275 Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys
276 385          390          395          400
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280          405          410
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284 <211> LENGTH: 1740
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286 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
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291 <222> LOCATION: (87)..(1445)
293 <400> SEQUENCE: 3
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297 Met Ala Gly Tyr Leu Arg Val Val Arg
298          1          5
300 tcg ctc tgc aga gcc tca ggc tcg cgg ccg gcc tgg gcg ccg gcg gcc 161
301 Ser Leu Cys Arg Ala Ser Gly Ser Arg Pro Ala Trp Ala Pro Ala Ala
302 10          15          20          25
304 ctg aca gcc ccc acc tcg caa gag cag ccg cgg cgc cac tat gcc gac 209
305 Leu Thr Ala Pro Thr Ser Gln Glu Gln Pro Arg Arg His Tyr Ala Asp
306          30          35          40
308 aaa agg atc aag gtg gcg aag ccc gtg gtg gag atg gat ggt gat gag 257
309 Lys Arg Ile Lys Val Ala Lys Pro Val Val Glu Met Asp Gly Asp Glu

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316	cac	gtg	gac	atc	cag	cta	aag	tat
317	His	Val	Asp	Ile	Gln	Leu	Lys	Tyr
318		75		80		85		
322	gac	cag	act	gat	gac	cag	gtc	acc
323	Asp	Gln	Thr	Asp	Asp	Gln	Val	Thr
324	90			95		100		105
326	aag	tac	agt	gtg	gct	gtc	aag	tgt
327	Lys	Tyr	Ser	Val	Ala	Val	Lys	Cys
328				110		115		120
330	cgt	gtg	gaa	gag	ttc	aag	ctg	aag
331	Arg	Val	Glu	Glu	Phe	Lys	Leu	Lys
332			125			130		135
334	act	atc	cgg	aac	atc	ctg	ggg	ggg
335	Thr	Ile	Arg	Asn	Ile	Leu	Gly	Gly
336		140				145		150
338	tgc	aaa	aac	atc	cca	cgc	cta	gtc
339	Cys	Lys	Asn	Ile	Pro	Arg	Leu	Val
340		155				160		165
342	att	ggc	agg	cac	gcc	cat	ggc	gac
343	Ile	Gly	Arg	His	Ala	His	Gly	Asp
344	170					175		180
346	gca	gac	cgg	gcc	ggc	act	ttc	aaa
347	Ala	Asp	Arg	Ala	Gly	Thr	Phe	Lys
348			190			195		200
350	agt	ggt	gtc	aag	gag	tgg	gaa	gtg
351	Ser	Gly	Val	Lys	Glu	Trp	Glu	Val
352			205			210		215
354	ggc	atg	ggc	atg	tac	aac	acc	gac
355	Gly	Met	Gly	Met	Tyr	Asn	Thr	Asp
356		220				225		230
358	agc	tgc	ttc	cag	tat	gcc	atc	cag
359	Ser	Cys	Phe	Gln	Tyr	Ala	Ile	Gln
360		235				240		245
362	acc	aag	aac	acc	ata	ctg	aaa	gcc
363	Thr	Lys	Asn	Thr	Ile	Leu	Lys	Ala
364	250					255		260
366	ttc	cag	gag	atc	ttt	gac	aag	cac
367	Phe	Gln	Glu	Ile	Phe	Asp	Lys	His
368			270			275		280
370	aag	atc	tgg	tat	gag	cac	cgg	ctc
371	Lys	Ile	Trp	Tyr	Glu	His	Arg	Leu
372			285			290		295
374	ctc	aag	tct	tcg	ggt	ggc	ttt	gtg
375	Leu	Lys	Ser	Ser	Gly	Gly	Phe	Val
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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date